

### **AMENDMENTS TO THE SPECIFICATION**

Please amend the paragraph beginning on page 60, line 7 as follows:

For the cyclic peptide SRGDGWS (**SEQ ID NO:57**), shown in Figure 16 (srgdgwsLowest5A.ps), there were 62 low energy conformers. There was one family of very similar conformers (yellow square at bottom left) and two families of quite similar conformers in yellow/white, one roughly in the middle of the graph, and one (with only moderately similar conformers) near the top right corner. These comprised approximately 20 of the 62 conformers. The rest of the low energy conformers were not very similar to each other, and much of the graph is red or black. Backbone overlaid conformers from most similar family, No. 1, are shown at the lower left. In the lower middle, is family No. 2. These conformers, when overlaid are clearly not similar. Conformers in family No. 3 (lower right) are rather heterogeneous, although not as much as those from the red and black regions of the graph.

Please amend the paragraph beginning on page 60, line 17 as follows:

For the cyclic peptide SRGPGWS (**SEQ ID NO:57**), representing the substitution of Pro for Asp 4, the graph of the lowest energy conformers looks quite different (FIG. 17; srgpgwsLowest5B.ps). There is a much larger family of very similar conformers (lower left of graph, family No. 1, conformers 1-26). Family No. 2 also has very similar conformers, although they are all different from family No. 1. Even family No. 3, representing over two thirds of all low energy conformers (frames 1-59) contains conformers that are similar enough to give a blurred donut appearance. Thus, substitution of a single pro for another residue (asp in this case) clearly freezes out two additional families of conformers. As this peptide has two glycines, the effect of proline on conformational narrowing of cyclic peptides with 1 or 0 glycines may be more profound.